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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

COLDREN ET AL.

CASE NO.: BC1019 US PCT

APPLICATION NO.: 10/069,425

GROUP ART UNIT: UNKNOWN

FILED: FEBRUARY 19, 2002

EXAMINER: UNKNOWN

FOR: CIS-PRENYLTRANSFERASES FROM PLANTS

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

DECLARATION IN ACCORDANCE WITH 37 CFR 1.821

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR 1.821(c) and (e), respectively are the same.

Respectfully submitted,

Md Fel
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Attorney for Applicant
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Dated:

7/26/02

I hereby certify that this paper is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to: U. S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202 on this date. July 26, 2002

Mary Beth Pitcher

Mary Beth Pitcher

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company

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<130> BC1019 PCT

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<150> 60/155,046

<151> 1999-09-21

<160> 37

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<213> Dimorphotheca

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<213> Calendula officinalis

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Glu Val Asp Phe Leu Met Glu Met Tyr Glu Asp Leu Leu Arg Thr Asp
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Tyr Ser Gly Lys Tyr Asp Ile Ile Glu Ala Cys Lys Ser Val Ala Thr
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Lys Val Lys Asp Gly Val Ile Ile Pro Lys Gln Ile Asp Glu Lys Tyr
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Phe Lys Gln Glu Leu Gly Thr Lys Met Ile Asp Phe Pro Tyr Pro Asp
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 35 40 45
 Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
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 85 90 95
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
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Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
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Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
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Ile Met Arg Ala Thr Ala Asn Asn Ser Lys Cys Val Leu Leu Ile Ala
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Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
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Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
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Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
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<213> Hevea brasiliensis

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 Lys His Lys Leu Pro Glu Gly Gly Gly His Lys Ala Gly Phe Leu Ala
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 Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Lys Pro His Glu
 85 90 95
 Val Gln Tyr Val Met Asp Leu Met Leu Glu Lys Ile Glu Gly Met Ile
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 Met Glu Glu Ser Ile Ile Asn Ala Tyr Asp Ile Cys Val Arg Phe Val
 115 120 125
 Gly Asn Leu Lys Leu Leu Ser Glu Pro Val Lys Thr Ala Ala Asp Lys
 130 135 140
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 Val Cys Tyr Thr Ser Thr Asp Glu Ile Val His Ala Val Glu Glu Ser
 165 170 175
 Ser Glu Leu Asn Ser Asn Glu Val Cys Asn Asn Gln Glu Leu Glu Glu
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 Ala Asn Ala Thr Gly Ser Ser Thr Val Ile Gln Thr Glu Asn Met Glu
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 Ser Tyr Ser Gly Ile Lys Leu Val Asp Leu Glu Lys Asn Thr Tyr Ile
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 Asn Pro Tyr Pro Asp Val Leu Ile Arg Thr Ser Gly Glu Thr Arg Leu
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 Ser Asn Tyr Leu Leu Trp Gln Thr Thr Asn Cys Ile Leu Tyr Ser Pro
 245 250 255
 Tyr Ala Leu Trp Pro Glu Ile Gly Leu Arg His Val Val Trp Ser Val
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Leu Lys
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Thr Ile Tyr Ala Phe Ser Ile Asp Asn Phe Arg Arg Gln Pro Arg Glu
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Val Gln Cys Val Met Asn Leu Met Met Glu Lys Ile Glu Glu Ile Ile
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Gly Asn Leu Asn Leu Leu Asp Glu Pro Ile Arg Ile Ala Ala Glu Lys
130 135 140

Ile Met Arg Ala Thr Ala Asn Asn Ser Gly Phe Val Leu Leu Ile Ala
 145 150 155 160
 Val Ala Tyr Ser Ser Thr Asp Glu Ile Gly His Ala Val Glu Glu Ser
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 Ser Lys Asp Lys Leu Asn Ser Asn Glu Val Cys Asn Asn Gly Ile Glu
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 Glu Lys His Lys Glu Tyr Leu Lys
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 35 40 45
 Thr Ala Lys Thr Asp Val Val Gly Glu Glu Glu Ala Arg Glu Val Asn
 50 55 60
 Glu Arg Ala Glu Glu Phe Pro Asp Gly Leu Arg Arg Glu Leu Met Pro
 65 70 75 80
 Glu His Val Ala Val Ile Met Asp Gly Asn Val Arg Trp Ala Gln Lys
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 Arg Gly Leu Pro Ala Ala Ser Gly His Gln Ala Gly Val Arg Ser Leu
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 Arg Glu Leu Val Glu Leu Cys Cys Lys Trp Gly Ile Lys Val Leu Ser
 115 120 125
 Val Phe Ala Phe Ser Tyr Asp Asn Trp Ser Arg Ser Glu Gly Glu Val
 130 135 140
 Gly Phe Leu Met Ser Leu Ile Glu Arg Val Val Lys Ala Glu Leu Pro
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 Ile Leu Gly Gly Lys Ala Phe Glu Cys Arg Asp Trp Gly Phe Val Lys
 165 170 175
 Ala Ser Glu Gln Leu Gln Leu Ile Ile Asp Val Glu Glu Thr Thr Lys
 180 185 190
 Glu Asn Ser Arg Leu Gln Phe Ile Val Ala Leu Ser Tyr Ser Gly Gln
 195 200 205
 Cys Asp Ile Leu Gln Ala Cys Lys Asn Ile Gly His Lys Val Lys Asp
 210 215 220
 Gly Leu Ile Glu Pro Glu Asp Ile Asn Lys Ser Leu Ile Glu Gln Glu
 225 230 235 240
 Leu Gln Thr Asn Cys Thr Glu Phe Pro Phe Pro Asp Leu Leu Ile Arg
 245 250 255
 Thr Ser Gly Glu Leu Arg Val Ser Asn Phe Met Leu Trp Gln Ile Ala
 260 265 270
 Tyr Thr Glu Leu Cys Phe Phe Ser Thr Leu Trp Pro Asp Phe Gly Lys
 275 280 285

Asp Glu Phe Val Glu Ala Leu Ser Ser Phe Gln Lys Arg Gln Arg Arg
 290 295 300

Tyr Gly Gly Arg Asn
 305

<210> 13
 <211> 1021
 <212> DNA
 <213> Oryza sativa

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 ggctctgggtc acaggggtggg cttctctgct ctcatgcca gcctgctcta ctgctatgaa 180
 atgggcgtga agtatatcac ggtgtatgca tttagcatcg ataattttaa gcgagatccg 240
 actgaggtga aatccttgat ggagttaatg gaggaaaaga tcaatgaact gctagaaaac 300
 agaaatgtca tcaacaaggt taactgtaag atcaacttct gggggaactt ggacatgttg 360
 agcaaatacg tgagggtagc agctgagaaa ctgatggcta ccactgctga aaacacggga 420
 ctggtcttct ctgtttgcat gccatacaac tccacttctg agattgtcaa tgcgggtcaat 480
 aaggtctgtg cagaaaggag ggatatactg cagagggagg atgctgacag tgttgcaaat 540
 aatggtgtgt attcagacat ttcagtggca gatctggacc gccatatgta cagcgctggg 600
 tgccccgatc ctgacattgt gatccggacc tcaggtgaga ctgcctgag caatttcctt 660
 ctgtggcaga cgacgttcag tcatttgtag aatccagacc ctctttggcc ggagttctct 720
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 tatgaaatat ataaaggata gctatgccat tgtatgcttg aacatgtgta tgcttgagtt 960
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 a 1021

<210> 14
 <211> 252
 <212> PRT
 <213> Oryza sativa

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 35 40 45
 Ile Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr
 50 55 60
 Glu Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu
 65 70 75 80
 Leu Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe
 85 90 95
 Trp Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu
 100 105 110

Lys Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val
 115 120 125
 Cys Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys
 130 135 140
 Val Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser
 145 150 155 160
 Val Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp
 165 170 175
 Arg His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg
 180 185 190
 Thr Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr
 195 200 205
 Phe Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe
 210 215 220
 Lys His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser
 225 230 235 240
 Ile Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 245 250

<210> 15
 <211> 900
 <212> DNA
 <213> *Oryza sativa*

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 gctgtcctct cgtatggccc aatgcctaag catattgcat ttattatgga tggtaaccgt 180
 agatatgcta aattcaggag tatccaggaa ggctctgggtc acaggggtggg cttctctgct 240
 ctcattgcca gcctgctcta ctgctatgaa atgggctgta agtatatcac ggtgtatgca 300
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 atcaacttct ggggggaactt ggacatgttg agcaaatacag tgagggtagc agctgagaaa 480
 ctgatggcta ccaactgctga aaacacggga ctggtcttct ctgtttgcat gccatacaac 540
 tccacttctg agattgtcaa tgcggtcaat aaggtctgtg cagaaaggag ggatatactg 600
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 tcaggtgaga ctgcctgag caatttcctt ctgtggcaga cgacgttcag tcatttgcag 780
 aatccagacc ctctttggcc ggagttctct ttcaagcacc ttgtctgggc catactccag 840
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<210> 16
 <211> 299
 <212> PRT
 <213> *Oryza sativa*

<400> 16
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 1 5 10 15

Glu Asn Thr Asp Glu Leu Ile Ala Thr Gly Val Leu Ala Ser Leu Gln
 20 25 30
 Asn Phe Ile Arg Lys Cys Ile Val Ala Val Leu Ser Tyr Gly Pro Met
 35 40 45
 Pro Lys His Ile Ala Phe Ile Met Asp Gly Asn Arg Arg Tyr Ala Lys
 50 55 60
 Phe Arg Ser Ile Gln Glu Gly Ser Gly His Arg Val Gly Phe Ser Ala
 65 70 75 80
 Leu Ile Ala Ser Leu Leu Tyr Cys Tyr Glu Met Gly Val Lys Tyr Ile
 85 90 95
 Thr Val Tyr Ala Phe Ser Ile Asp Asn Phe Lys Arg Asp Pro Thr Glu
 100 105 110
 Val Lys Ser Leu Met Glu Leu Met Glu Glu Lys Ile Asn Glu Leu Leu
 115 120 125
 Glu Asn Arg Asn Val Ile Asn Lys Val Asn Cys Lys Ile Asn Phe Trp
 130 135 140
 Gly Asn Leu Asp Met Leu Ser Lys Ser Val Arg Val Ala Ala Glu Lys
 145 150 155 160
 Leu Met Ala Thr Thr Ala Glu Asn Thr Gly Leu Val Phe Ser Val Cys
 165 170 175
 Met Pro Tyr Asn Ser Thr Ser Glu Ile Val Asn Ala Val Asn Lys Val
 180 185 190
 Cys Ala Glu Arg Arg Asp Ile Leu Gln Arg Glu Asp Ala Asp Ser Val
 195 200 205
 Ala Asn Asn Gly Val Tyr Ser Asp Ile Ser Val Ala Asp Leu Asp Arg
 210 215 220
 His Met Tyr Ser Ala Gly Cys Pro Asp Pro Asp Ile Val Ile Arg Thr
 225 230 235 240
 Ser Gly Glu Thr Arg Leu Ser Asn Phe Leu Leu Trp Gln Thr Thr Phe
 245 250 255
 Ser His Leu Gln Asn Pro Asp Pro Leu Trp Pro Glu Phe Ser Phe Lys
 260 265 270
 His Leu Val Trp Ala Ile Leu Gln Tyr Gln Arg Val His Pro Ser Ile
 275 280 285
 Glu Gln Ser Arg Asn Leu Ala Lys Lys Gln Leu
 290 295

<210> 17
 <211> 1028
 <212> DNA
 <213> Glycine max

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<400> 17
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attctcacta ttatcactat cgttatcggt atcggttgta tcatcctttc catcacggtt 180
cccaaacaca gagtcttata gtctcgaagc gcggttccgc cattgcgaag tgtcacgctg 240
atagcgtgac acttcgtgat gacggagtct cgctcgccca agagtcgttg gagccacttc 300
cggcggaaact cgcggcggag atgatgccga agcatgtggc ggtgataatg gacgggaacg 360
ggaggtgggc gaaggtgaag gggctgccac catcggcggg gcaccaggcg ggggtgcaat 420
cgctgaggaa aatggtgagg ctgtgttgca gctggggaat taaggttcta acggttttcg 480
cgttctctac ggataactgg gttcgcccca aggtggaggt tgatttcttg atgaggctgt 540
ttgagagaac aataaactct gaagttcaaa cttttaagag ggaaggaatt agaatatctg 600
tgattggaga ttcataaagg ttgcctgagt ctttaaaaag aatgatagct agtgagaag 660
aggatacaaa acaaaattcg agattccaac ttattgtggc agtgggatac agtggaaaat 720
atgatgttgt gcaagcatgt aaaagtgtag ccaagaaagt caaagatggt cacattcact 780
tggatgacat aaacgaaaac attattgaac aagaattgga aactaattgt actgagtttc 840
cttatcctga tctactaata cgaactagtg gcgagcttag agtgagtaac ttctgttgt 900
ggcaattagc ctacacagaa ctttatttta atcgggaact ctggccagat tttgggaagg 960
atgagtttgt agatgcatta agttcatttc aacaaagaca aagacgctat ggtggtcgac 1020
attcataa 1028

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<210> 18
<211> 322
<212> PRT
<213> Glycine max

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<400> 18
Met Phe Ser Leu Arg Leu Pro Ile Pro Leu Val Lys Thr Pro Pro Ser
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Pro Ser Cys Tyr Tyr Ser His Tyr Tyr His Tyr Arg Tyr Arg Tyr Arg
20 25 30
Cys Tyr His Pro Phe His His Arg Ser Gln Thr Gln Ser Leu Ile Val
35 40 45
Ser Lys Arg Gly Ser Ala Ile Ala Lys Cys His Ala Asp Ser Val Thr
50 55 60
Leu Arg Asp Asp Gly Val Ser Leu Ala Gln Glu Ser Leu Glu Pro Leu
65 70 75 80
Pro Ala Glu Leu Ala Ala Glu Met Met Pro Lys His Val Ala Val Ile
85 90 95
Met Asp Gly Asn Gly Arg Trp Ala Lys Val Lys Gly Leu Pro Pro Ser
100 105 110
Ala Gly His Gln Ala Gly Val Gln Ser Leu Arg Lys Met Val Arg Leu
115 120 125
Cys Cys Ser Trp Gly Ile Lys Val Leu Thr Val Phe Ala Phe Ser Thr
130 135 140
Asp Asn Trp Val Arg Pro Lys Val Glu Val Asp Phe Leu Met Arg Leu
145 150 155 160
Phe Glu Arg Thr Ile Asn Ser Glu Val Gln Thr Phe Lys Arg Glu Gly
165 170 175

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Ile Arg Ile Ser Val Ile Gly Asp Ser Ser Arg Leu Pro Glu Ser Leu
180 185 190

Lys Arg Met Ile Ala Ser Ala Glu Glu Asp Thr Lys Gln Asn Ser Arg
195 200 205

Phe Gln Leu Ile Val Ala Val Gly Tyr Ser Gly Lys Tyr Asp Val Val
210 215 220

Gln Ala Cys Lys Ser Val Ala Lys Lys Val Lys Asp Gly His Ile His
225 230 235 240

Leu Asp Asp Ile Asn Glu Asn Ile Ile Glu Gln Glu Leu Glu Thr Asn
245 250 255

Cys Thr Glu Phe Pro Tyr Pro Asp Leu Leu Ile Arg Thr Ser Gly Glu
260 265 270

Leu Arg Val Ser Asn Phe Leu Leu Trp Gln Leu Ala Tyr Thr Glu Leu
275 280 285

Tyr Phe Asn Arg Glu Leu Trp Pro Asp Phe Gly Lys Asp Glu Phe Val
290 295 300

Asp Ala Leu Ser Ser Phe Gln Gln Arg Gln Arg Arg Tyr Gly Gly Arg
305 310 315 320

His Ser

<210> 19

<211> 1026

<212> DNA

<213> Triticum aestivum

<400> 19

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gggaactcgc	ggtgggcggc	agcgcggggc	ctgccgccga	cggacgggca	cgagcacggg	180
atgcgcgcgc	tgatgaggac	ggtgcggctc	tcccgcgcct	ggggcatccg	cgtcctcacc	240
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gccttgatcg	agaggtttat	caacgacaac	ctcgccgagt	tcttgaggga	agggacccgt	360
ctacgtataa	tcggtgaccg	ctcaaggctg	ccgatctctg	tgacagaagac	tgacagagac	420
gccgaggagg	caacaagaaa	caactcgacg	ctcgatctag	tcctagccat	cagctacagc	480
gggcgaatgg	acattgtgca	ggcatgcccg	aatctcgccc	agaaagtgga	cgccaagctg	540
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tcttgcccgg	acctgctcat	caggaccagc	ggcgagctga	ggctgagcaa	cttcctgcta	660
tggcagtcgg	cttactcgga	gctcttcttc	accgacacgc	tctggcctga	tttcggggag	720
gcccgaatag	tccaagccat	gatggccttc	cagagcagag	acaggcgctt	tggaagaaga	780
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ctcaagatgc	gtggtgtact	ataggagagg	ctactaaaac	ttctctccag	tgattttact	960
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<210> 20

<211> 266

<212> PRT

<213> Triticum aestivum

<400> 20

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Ala Ala Glu Glu Leu Leu Ser Gln Gly Leu Arg Ala Glu Ser Leu Pro
      20              25              30

Arg His Val Ala Leu Val Met Asp Gly Asn Ser Arg Trp Ala Ala Ala
      35              40              45

Arg Gly Leu Pro Pro Thr Asp Gly His Glu His Gly Met Arg Ala Leu
      50              55              60

Met Arg Thr Val Arg Leu Ser Arg Ala Trp Gly Ile Arg Val Leu Thr
      65              70              75              80

Ala Phe Gly Phe Ser Leu Glu Asn Trp Asn Arg Pro Lys Ala Glu Val
      85              90              95

Asp Phe Leu Met Ala Leu Ile Glu Arg Phe Ile Asn Asp Asn Leu Ala
      100             105             110

Glu Phe Leu Arg Glu Gly Thr Arg Leu Arg Ile Ile Gly Asp Arg Ser
      115             120             125

Arg Leu Pro Ile Ser Val Gln Lys Thr Ala Arg Asp Ala Glu Glu Ala
      130             135             140

Thr Arg Asn Asn Ser Gln Leu Asp Leu Val Leu Ala Ile Ser Tyr Ser
      145             150             155             160

Gly Arg Met Asp Ile Val Gln Ala Cys Arg Asn Leu Ala Gln Lys Val
      165             170             175

Asp Ala Lys Leu Leu Arg Pro Glu Asp Ile Asp Glu Ser Leu Phe Ala
      180             185             190

Asp Glu Leu Gln Thr Ser Glu Thr Ser Cys Pro Asp Leu Leu Ile Arg
      195             200             205

Thr Ser Gly Glu Leu Arg Leu Ser Asn Phe Leu Leu Trp Gln Ser Ala
      210             215             220

Tyr Ser Glu Leu Phe Phe Thr Asp Thr Leu Trp Pro Asp Phe Gly Glu
      225             230             235             240

Ala Gln Tyr Leu Gln Ala Met Met Ala Phe Gln Ser Arg Asp Arg Arg
      245             250             255

Phe Gly Arg Arg Lys Asn Asn Ala Ala Leu
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<210> 21

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Domain I of
published alignment

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 <222> (2)..(3)
 <223> X = any amino acid

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 <222> (8)
 <223> X = any amino acid

<220>
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 <222> (10)
 <223> X = any amino acid

<300>
 <301> Apfel, C. M.
 <302> Use of Genomincs to Indentify Bacterial Undecaprenyl
 Pyrophosphate Synthetase: Clooning, Expression, and
 Characterization of the Essential uppS Gene
 <303> J. Bacteriol.
 <304> 81
 <306> 483-492
 <307> 1999

<400> 21
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<210> 22
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Domain V of published
 alignment

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 <222> (3)
 <223> X = any amino acid

<220>
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<220>
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<400> 22
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Leu Trp Gln Xaa Xaa Tyr Xaa Glu
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<210> 23
 <211> 750
 <212> DNA
 <213> Micrococcus luteus

<300>
 <301> Shimizu, N.
 <302> Molecular Cloning, Expression, and Purification of Undecprenyl
 Diphosphate Synthase: No Sequence Similarity between E- and
 Z-prenyl Diphosphate Synthases
 <303> J. Biol. Chem.
 <304> 273
 <306> 19476-19481
 <307> 1998

<400> 23
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 ccgcgcataa aaggacatta tgaaggcatg cagaccgtaa agaaaatcac aagatatgct 180
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 cctaaagatg aggttaatta cttgatgaaa ctaccgggtg atttttttaa cacattttta 300
 ccggaactca ttgaaaaaaa tgttaaagtt gaaacgattg gctttattga tgatttaccg 360
 gaccatacaa aaaaagcagt gttagaagcg aaagagaaaa cgaaacataa tacagggttta 420
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 aatgaatatt tatttacagc aaatatgcct gatcctgagt tgtaatcag aacttccggg 600
 gaagaacggt taagtaactt ttttaattgg caatgttcat atagtgagtt tgtatttata 660
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<210> 24
 <211> 249
 <212> PRT
 <213> Micrococcus luteus

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 20 25 30
 Arg Trp Ala Lys Gln Lys Lys Met Pro Arg Ile Lys Gly His Tyr Glu
 35 40 45
 Gly Met Gln Thr Val Lys Lys Ile Thr Arg Tyr Ala Ser Asp Leu Gly
 50 55 60
 Val Lys Tyr Leu Thr Leu Tyr Ala Phe Ser Thr Glu Asn Trp Ser Arg

65		70		75		80
Pro Lys Asp Glu Val Asn Tyr Leu Met Lys Leu Pro Gly Asp Phe Leu						
	85			90		95
Asn Thr Phe Leu Pro Glu Leu Ile Glu Lys Asn Val Lys Val Glu Thr						
	100		105		110	
Ile Gly Phe Ile Asp Asp Leu Pro Asp His Thr Lys Lys Ala Val Leu						
	115		120		125	
Glu Ala Lys Glu Lys Thr Lys His Asn Thr Gly Leu Thr Leu Val Phe						
	130		135		140	
Ala Leu Asn Tyr Gly Gly Arg Lys Glu Ile Ile Ser Ala Val Gln Leu						
	145		150		155	160
Ile Ala Glu Arg Tyr Lys Ser Gly Glu Ile Ser Leu Asp Glu Ile Ser						
	165		170		175	
Glu Thr His Phe Asn Glu Tyr Leu Phe Thr Ala Asn Met Pro Asp Pro						
	180		185		190	
Glu Leu Leu Ile Arg Thr Ser Gly Glu Glu Arg Leu Ser Asn Phe Leu						
	195		200		205	
Ile Trp Gln Cys Ser Tyr Ser Glu Phe Val Phe Ile Asp Glu Phe Trp						
	210		215		220	
Pro Asp Phe Asn Glu Glu Ser Leu Ala Gln Cys Ile Ser Ile Tyr Gln						
	225		230		235	240
Asn Arg His Arg Arg Phe Gly Gly Leu						
	245					

<210> 25

<211> 861

<212> DNA

<213> *Saccharomyces cerevisiae*

<300>

<308> AB013497

<400> 25

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gggaacagga	gattcgctag	aaagaaagag	atggacgtaa	aggagggcca	cgaggcagga	180
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gttcggggtg	ctgtggaaac	tacaaagaac	aacaaaaggg	ccacgttaaa	tatctgcttt	480
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aagggcgcgc	ctatagacga	aagcacgtta	gaatcgcac	tctacacggc	gggggtaccc	600
ccttttagatt	tattgattag	gacaagtggc	gtttccagat	taagtgactt	tttgatatgg	660
caggcatcga	gtaagggcgt	acgcacgaa	ttgctggatt	gtttatggcc	agagtttggg	720
cctatacggg	tggtcatggat	tttattaaaa	ttttcgtttc	acaaatcctt	tttaacaaa	780
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<210> 26
 <211> 286
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 26
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 20 25 30
 Arg His Val Gly Phe Ile Met Asp Gly Asn Arg Arg Phe Ala Arg Lys
 35 40 45
 Lys Glu Met Asp Val Lys Glu Gly His Glu Ala Gly Phe Val Ser Met
 50 55 60
 Ser Arg Ile Leu Glu Leu Cys Tyr Glu Ala Gly Val Asp Thr Ala Thr
 65 70 75 80
 Val Phe Ala Phe Ser Ile Glu Asn Phe Lys Arg Ser Ser Arg Glu Val
 85 90 95
 Glu Ser Leu Met Thr Leu Ala Arg Glu Arg Ile Arg Gln Ile Thr Glu
 100 105 110
 Arg Gly Glu Leu Ala Cys Lys Tyr Gly Val Arg Ile Lys Ile Ile Gly
 115 120 125
 Asp Leu Ser Leu Leu Asp Lys Ser Leu Leu Glu Asp Val Arg Val Ala
 130 135 140
 Val Glu Thr Thr Lys Asn Asn Lys Arg Ala Thr Leu Asn Ile Cys Phe
 145 150 155 160
 Pro Tyr Thr Gly Arg Glu Glu Ile Leu His Ala Met Lys Glu Thr Ile
 165 170 175
 Val Gln His Lys Lys Gly Ala Ala Ile Asp Glu Ser Thr Leu Glu Ser
 180 185 190
 His Leu Tyr Thr Ala Gly Val Pro Pro Leu Asp Leu Leu Ile Arg Thr
 195 200 205
 Ser Gly Val Ser Arg Leu Ser Asp Phe Leu Ile Trp Gln Ala Ser Ser
 210 215 220
 Lys Gly Val Arg Ile Glu Leu Leu Asp Cys Leu Trp Pro Glu Phe Gly
 225 230 235 240
 Pro Ile Arg Met Ala Trp Ile Leu Leu Lys Phe Ser Phe His Lys Ser
 245 250 255
 Phe Leu Asn Lys Glu Tyr Arg Leu Glu Glu Gly Asp Tyr Asp Glu Glu
 260 265 270
 Thr Asn Gly Asp Pro Ile Asp Leu Lys Glu Lys Lys Leu Asn
 275 280 285

<210> 27
 <211> 1032
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<300>
 <308> AB013498

<400> 27
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 ttaagggtag ggccagtgcc tgaacatgtc tcctttatca tggatggtaa ccggagatat 240
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 Phe Tyr Val Asn Leu Gln Asn Ile Leu Ile Lys Ala Leu Arg Val Gly
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 Pro Val Pro Glu His Val Ser Phe Ile Met Asp Gly Asn Arg Arg Tyr
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 Cys Val Ser Ala Tyr Ala Phe Ser Ile Glu Asn Phe Asn Arg Pro Lys
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 225 230 235 240
 Lys Cys Glu Leu Leu Ile Arg Thr Ser Gly His Arg Arg Leu Ser Asp
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 Tyr Met Leu Trp Gln Val His Glu Asn Ala Thr Ile Glu Phe Ser Asp
 260 265 270
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 Lys Trp Ser Phe Phe Ser Thr Ile Gln Lys Tyr Asn Glu Lys Asn His
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